

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING  
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/050,216  
Source: O1PE  
Date Processed by STIC: 2/6/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

**Raw Sequence Listing Error Summary**

| <u>ERROR DETECTED</u>   | <u>SUGGESTED CORRECTION</u>  | <u>SERIAL NUMBER:</u> <u>10/050,216</u> |
|---|--|---|
| <b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b> |  |   |
| 1 <input type="checkbox"/> Wrapped Nucleic<br>Wrapped Aminos  | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."   |   |
| 2 <input type="checkbox"/> Invalid Line Length  | The rules require that a line not exceed 72 characters in length. This includes white spaces.  |   |
| 3 <input type="checkbox"/> Misaligned Amino<br>Numbering  | The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.  |   |
| 4 <input type="checkbox"/> Non-ASCII  | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.   |   |
| 5 <input checked="" type="checkbox"/> Variable Length   | Sequence(s) <u>7</u> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.  |   |
| 6 <input type="checkbox"/> PatentIn 2.0<br>"bug"  | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <u>      </u> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |   |
| 7 <input type="checkbox"/> Skipped Sequences<br>(OLD RULES)   | Sequence(s) <u>      </u> missing. If intentional, please insert the following lines for each skipped sequence:<br>(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)<br>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>This sequence is intentionally skipped                          |   |
|   | Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.  |   |
| 8 <input type="checkbox"/> Skipped Sequences<br>(NEW RULES)   | Sequence(s) <u>      </u> missing. If Intentional, please insert the following lines for each skipped sequence.<br><210> sequence id number<br><400> sequence id number<br>000   |   |
| 9 <input type="checkbox"/> Use of n's or Xaa's<br>(NEW RULES)   | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.   |   |
| 10 <input type="checkbox"/> Invalid <213><br>Response   | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence  |   |
| 11 <input type="checkbox"/> Use of <220>  | Sequence(s) <u>      </u> missing the <220> "Feature" and associated numeric identifiers and responses.<br>Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.<br>(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)                                    |   |
| 12 <input type="checkbox"/> PatentIn 2.0<br>"bug"   | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.  |   |
| 13 <input type="checkbox"/> Misuse of n   | n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.  |   |



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/050,216

DATE: 02/06/2002  
TIME: 19:11:09

Input Set : A:\SEQUENCE LISTING.txt  
Output Set: N:\CRF3\02062002\J050216.raw

Does Not Comply  
Corrected Filing Number

4 <110> APPLICANT: Curtis, Rory A.J., Lora, Jose M.  
6 <120> TITLE OF INVENTION: 46798, A HUMAN MATRIX METALLOPROTEINASE  
7 AND USES THEREFOR  
9 <130> FILE REFERENCE: MPI2001-014P1RCP1(M)  
11 <140> CURRENT APPLICATION NUMBER: US/10/050,216  
11 <141> CURRENT FILING DATE: 2002-01-16  
11 <160> NUMBER OF SEQ ID NOS: 10  
13 <170> SOFTWARE: FastSEQ for Windows Version 3.0

## ERRORED SEQUENCES

224 <210> SEQ ID NO: 3  
225 <211> LENGTH: 1335  
226 <212> TYPE: DNA  
227 <213> ORGANISM: Homo sapiens  
229 <220> FEATURE:  
230 <221> NAME/KEY: CDS  
231 <222> LOCATION: (1)...(1335)  
233 <400> SEQUENCE: 3  
E--> 234 atg gtc gcg cgc gtc ctc ctg ctg cgc gcc ctg cag ctg cta ctg  
235 Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu Gln Leu Leu  
236 1 5 10 15  
E--> 238 tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga ggc cag gag ctg  
239 Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu  
240 20 25 30  
E--> 242 cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa  
243 Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu  
244 35 40 45  
E--> 246 cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga  
247 Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg  
248 50 55 60  
E--> 250 gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtc ttg gac cgc  
251 Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg  
252 65 70 75 80  
E--> 254 gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc  
255 Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr  
256 85 90 95  
E--> 258 aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga  
259 Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg  
260 100 105 110  
E--> 262 cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggg ggc  
263 His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly

ppr 1-3

1-5

Suggestion:  
Consult  
Sequence Ruler  
for valid format

48 Insert cumulative  
base totals  
at right margin of  
each line

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/050,216

DATE: 02/06/2002  
TIME: 19:11:09

Input Set : A:\SEQUENCE LISTING.txt  
Output Set: N:\CRF3\02062002\J050216.raw

264 115 120 125  
E--> 266 gcc ctg gcg cac gcc ttc ctg ccc cgc cgc ggc gaa gcg cac ttc gac  
267 Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp  
268 130 135 140  
E--> 270 caa gat gag cgc tgg tcc ctg agc cgc cgc ggg cgc aac ctg ttc  
271 Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe  
272 145 150 155 160  
E--> 274 gtg gtg ctg gcg cac gag atc ggt cac acg ctt ggc ctc acc cac tcg  
275 Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly Leu Thr His Ser  
276 165 170 175  
E--> 278 ccc gcg cgc gcg ctc atg gcg ccc tac tac aag agg ctg ggc cgc  
279 Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg  
280 180 185 190  
E--> 282 gac gcg ctg ctc agc tgg gac gac gtg ctg gcc gtg cag agc ctg tat  
283 Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr  
284 195 200 205  
E--> 286 ggg aag ccc cta ggg ggc tca gtg gcc gtc cag ctc cca gga aag ctg  
287 Gly Lys Pro Leu Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu  
288 210 215 220  
E--> 290 ttc act gac ttt gag acc tgg gac tcc tac agc ccc caa gga agg cgc  
291 Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg  
292 225 230 235 240  
E--> 294 cct gaa acg cag ggc cct aaa tac tgc cac tct tcc ttc gat gcc atc  
295 Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile  
296 245 250 255  
E--> 298 act gta gac agg caa cag caa ctg tac att ttt aaa ggg agc cat ttc  
299 Thr Val Asp Arg Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe  
300 260 265 270  
E--> 302 tgg gag gtg gca gct gat ggc aac gtc tca gag ccc cgt cca ctg cag  
303 Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln  
304 275 280 285  
E--> 306 gaa aga tgg gtc ggg ctg ccc ccc aac att gag gct gcg gca gtg tca  
307 Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala Ala Val Ser  
308 290 295 300  
E--> 310 ttg aat gat gga gat ttc tac ttc aaa ggg ggt cga tgc tgg agg  
311 Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg  
312 305 310 315 320  
E--> 314 ttc cgg ggc ccc aag cca gtg tgg ggt ctc cca cag ctg tgc cgg gca  
315 Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala  
316 325 330 335  
E--> 318 ggg ggc ctg ccc cgc cat cct gac gcc gcc ctc ttc cct cct ctg  
319 Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu  
320 340 345 350  
E--> 322 cgc cgc ctc atc ctc ttc aag ggt gcc cgc tac tac gtg ctg gcc cga  
323 Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg  
324 355 360 365  
E--> 326 ggg gga ctg caa gtg gag ccc tac tac ccc cga agt ctg cag gac tgg  
327 Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp  
328 370 375 380

*present*  
*Cumulative*  
*base totals*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/050,216

DATE: 02/06/2002  
TIME: 19:11:19

Input Set : A:\SEQUENCE LISTING.txt  
Output Set: N:\CRF3\02062002\J050216.raw

E--> 330 gga ggc atc cct gag gag gtc agc ggc gcc ctg ccg agg ccc gat ggc  
331 Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly  
332 385 390 395 400  
E--> 334 tcc atc atc ttc ttc cga gat gac cgc tac tgg cgc ctc gac cag gcc  
335 Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala  
336 405 410 415  
E--> 338 aaa ctg cag gca acc acc tcg ggc cgc tgg gcc acc gag ctg ccc tgg  
339 Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp  
340 420 425 430  
E--> 342 atg ggc tgc tgg cat gcc aac tcg ggg agc gcc ctg ttc  
343 Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu Phe  
344 435 440 445  
391 <210> SEQ ID NO: 6  
392 <211> LENGTH: 471  
393 <212> TYPE: PRT  
394 <213> ORGANISM: Homo sapiens  
395 <200> P. 4  
396 <400> SEQUENCE: 6  
397 Met His Pro Gly Val Leu Ala Ala Phe Leu Phe Leu Ser Trp Thr His  
398 1 5 10 15  
399 Cys Arg Ala Leu Pro Leu Pro Ser Gly Gly Asp Glu Asp Asp Leu Ser  
400 20 25 30  
401 Glu Glu Asp Leu Gln Phe Ala Glu Arg Tyr Leu Arg Ser Tyr Tyr His  
402 35 40 45  
403 Pro Thr Asn Leu Ala Gly Ile Leu Lys Glu Asn Ala Ala Ser Ser Met  
404 50 55 60  
405 Thr Glu Arg Leu Arg Glu Met Gln Ser Phe Phe Gly Leu Glu Val Thr  
406 65 70 75 80  
407 Gly Lys Leu Asp Asp Asn Thr Leu Asp Val Met Lys Lys Pro Arg Cys  
408 85 90 95  
409 Gly Val Pro Asp Val Gly Glu Tyr Asn Val Phe Pro Arg Thr Leu Lys  
410 100 105 110  
411 Trp Ser Lys Met Asn Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp  
412 115 120 125  
413 Met Thr His Ser Glu Val Glu Lys Ala Phe Lys Lys Ala Phe Lys Val  
414 130 135 140  
415 Trp Ser Asp Val Thr Pro Leu Asn Phe Thr Arg Leu His Asp Gly Ile  
416 145 150 155 160  
417 Ala Asp Ile Met Ile Ser Phe Gly Ile Lys Glu His Gly Asp Phe Tyr  
418 165 170 175  
419 Pro Phe Asp Gly Pro Ser Gly Leu Leu Ala His Ala Phe Pro Pro Gly  
420 180 185 190  
421 Pro Asn Tyr Gly Gly Asp Ala His Phe Asp Asp Asp Glu Thr Trp Thr  
422 195 200 205  
423 Ser Ser Lys Gly Tyr Asn Leu Phe Leu Val Ala Ala His Glu Phe  
424 210 215 220  
425 Gly His Ser Leu Gly Leu Asp His Ser Lys Asp Pro Gly Ala Leu Met  
426 225 230 235 240  
427 Phe Pro Ile Tyr Thr Tyr Gly Lys Ser His Phe Met Leu Pro Asp  
428 245 250 255

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/050,216

DATE: 02/06/2002  
TIME: 19:11:09

Input Set : A:\SEQUENCE LISTING.txt  
Output Set: N:\CRF3\02062002\J050216.raw

429 Asp Asp Val Gln Gly Ile Gln Ser Leu Tyr Gly Pro Gly Asp Glu Asp  
 430 260 265 270  
 431 Pro Asn Pro Lys His Pro Lys Thr Pro Asp Lys Cys Asp Pro Ser Leu  
 432 275 280 285  
 433 Ser Leu Asp Ala Ile Thr Ser Leu Arg Gly Glu Thr Met Ile Phe Lys  
 434 290 295 300  
 435 Asp Arg Phe Phe Trp Arg Leu His Pro Gln Gln Val Asp Ala Glu Leu  
 436 305 310 315 320  
 437 Phe Leu Thr Lys Ser Phe Trp Pro Glu Leu Pro Asn Arg Ile Asp Ala  
 438 325 330 335  
 439 Ala Tyr Glu His Pro Ser His Asp Leu Ile Phe Arg Gly Arg  
 440 340 345 350  
 441 Lys Phe Trp Ala Leu Asn Gly Tyr Asp Ile Leu Glu Gly Tyr Pro Lys  
 442 355 360 365  
 443 Lys Ile Ser Glu Leu Gly Leu Pro Lys Glu Val Lys Lys Ile Ser Ala  
 444 370 375 380  
 445 Ala Val His Phe Glu Asp Thr Gly Lys Thr Leu Leu Phe Ser Gly Asn  
 446 385 390 395 400  
 447 Gln Val Trp Arg Tyr Asp Asp Thr Asn His Ile Met Asp Lys Asp Tyr  
 448 405 410 415  
 449 Pro Arg Leu Ile Glu Glu Asp Phe Pro Gly Ile Gly Asp Lys Val Asp  
 450 420 425 430  
 451 Ala Val Tyr Glu Lys Asn Gly Tyr Ile Tyr Phe Phe Asn Gly Pro Ile  
 452 435 440 445  
 453 Gln Phe Glu Tyr Ser Ile Trp Ser Asn Arg Ile Val Arg Val Met Pro  
 454 450 455 460  
 455 Ala Asn Ser Ile Leu Trp Cys  
 456 465 470

458 <211> LENGTH: 756 → 2207 insert this mandatory residue  
see item 5

459 <212> TYPE: PRT  
460 <213> ORGANISM: Homo sapiens 2207 insert this whenever 2217, 2227, or  
on Error 462 <223> OTHER INFORMATION: The X at positions 2-5 can be any amino acid.  
Summary 464 <223> OTHER INFORMATION: The amino acid at position 7 can be as few as 21, 2237  
sheet 465 up to 25, amino acids, and the amino acid can be is present  
466 any amino acid.

468 <223> OTHER INFORMATION: The X at positions 9-12 can be any amino acid.

470 <223> OTHER INFORMATION: The X at position 16 can be any amino acid.

472 <223> OTHER INFORMATION: The X at position 18 can be any amino acid.

474 <223> OTHER INFORMATION: The X at positions 21-22 can be any amino acid.

476 <223> OTHER INFORMATION: The X at positions 25-26 can be any amino acid.

478 <223> OTHER INFORMATION: The X at positions 27-28 can be any amino acid.

480 <223> OTHER INFORMATION: The amino acid at position 37 can be as few as 26, 28-29

481 up to 71, amino acids, and the amino acid can be what about X at position 35?

482 any amino acid.

484 <223> OTHER INFORMATION: The X at position 39 can be any amino acid.

486 <223> OTHER INFORMATION: The X at position 42 can be any amino acid.

488 <223> OTHER INFORMATION: The X at position 48 can be any amino acid.

490 <223> OTHER INFORMATION: The amino acid at position 50 can be as few as 4, 35?

491 up to 87 amino acids, and the amino acid can be

item 5

See P. 5

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/050,216

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Input Set : A:\SEQUENCE LISTING.txt  
Output Set: N:\CRF3\02062002\J050216.raw

492 any amino acid.  
494 <223> OTHER INFORMATION: The X at position 52 can be any amino acid.  
496  
E--> 496 <400> SEQUENCE: 7  
W--> 497 Leu Xaa Xaa Xaa Xaa Tyr Xaa Gln Xaa Xaa Xaa Xaa Leu Pro Val Xaa  
498 1 5 10 15  
W--> 499 Gly Xaa Leu Asp Xaa Xaa Thr Leu Xaa Xaa Met Xaa Xaa Pro Arg Cys  
500 20 25 30  
W--> 501 Gly Val Xaa Asp Xaa Phe Xaa Gly Gly Xaa Leu Ala His Ala Phe Xaa  
502 35 40 45  
W--> 503 Pro Xaa Gly Xaa Ala His Phe Asp  
E--> 504 50  
E--> 508 <210> SEQ ID NO: 8

55<-number the amino acids under every 5  
amino acids.

DO NOT use TAB  
codes between  
the numbers;  
use space characters

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/050,216

DATE: 02/06/2002  
TIME: 19:11:10

Input Set : A:\SEQUENCE LISTING.txt  
Output Set: N:\CRF3\02062002\J050216.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:234 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:3  
M:254 Repeated in SeqNo=3  
L:496 M:282 W: Numeric Field Identifier Missing, <210> is required.  
L:496 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:6 differs:7  
L:497 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:497 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7  
L:497 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7  
L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0  
L:499 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:499 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7  
L:499 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7  
L:499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0  
L:501 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:501 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7  
L:501 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7  
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0  
L:503 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:503 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7  
L:503 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7  
L:503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0  
L:504 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7  
L:504 M:252 E: No. of Seq. differs, <211>LENGTH:Input:7 Found:56 SEQ:0  
L:508 M:214 E: (33) Seq.# missing, SEQ ID NO:7